

SEQUENCE LISTING



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<110> Cashman, John R.
Lomri, Nouredine

<120> DNA SEQUENCE ENCODING FLAVIN-CONTAINING MONOOXYGENASE

<130> 16663-1-2

<140> 09/583,310

<141> 2000-05-30

<150> 08/617,671

<151> 1996-03-27

<150> 08/023,843

<151> 1993-02-26

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA probe
complementary to pig liver FMO

<400> 1

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<210> 2

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA probe
complementary to pig liver FMO

<400> 2

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<210> 3
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: AflIII site of
 5' HLFMO-3 cDNA

<400> 3
 ggtaccacat gtccatgggg aagaaag 27

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sal I site &
 13 NT seq complementary to 3' end HLFMO-3 cDNA

<400> 4
 gacgtcgacg gacccctagg tcaacaca 28

<210> 5
 <211> 1599
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 tcc atc agg agc tgt ctg gaa gag ggg ctg gag ccc acc tgc ttt gag 96
 Ser Ile Arg Ser Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu
 20 25 30
 aag agc aat gac att ggg ggc ctg tgg aaa ttt tca gac cat gca gag 144
 Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu
 35 40 45

gag ggc agg gct agc att tac aaa tca gtc ttt tcc aac tct tcc aaa	192
Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys	
50 55 60	
gag atg atg tgt ttc cca gac ttc cca ttt ccc gat gac ttc ccc aac	240
Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn	
65 70 75 80	
ttt atg cac aac agc aag atc cag gaa tat atc att gca ttt gcc aaa	288
Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys	
85 90 95	
gaa aag aac ctc ctg aag tac ata caa ttt aag aca ttt gta tcc agt	336
Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser	
100 105 110	
gta aat aaa cat cct gat ttt gca act act ggc cag tgg gat gtt acc	384
Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr	
115 120 125	
act gaa agg gat ggt aaa aaa gaa tcg gct gtc ttt gat gct gta atg	432
Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met	
130 135 140	
gtt tgt tcc gga cat cat gtg tat ccc aac cta cca aaa aag tcc ttt	480
Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Lys Ser Phe	
145 150 155 160	
cca gga cta aac cac ttt aaa ggc aaa tgc ttc cac agc agg gac tat	528
Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr	
165 170 175	
aaa gaa cca ggt gta ttc aat gga aag cgt gtc ctg gtg gtt ggc ctg	576
Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu	
180 185 190	
ggg aat tcg ggc tgt gat att gcc aca gaa ctc agc cgc aca gca gaa	624
Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu	
195 200 205	
cag gtc atg atc agt tcc aga agt ggc tcc tgg gtg atg agc cgg gtc	672
Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val	
210 215 220	
tgg gac aat ggt tat cct tgg gac atg ctg ctc gtc act cga ttt gga	720
Trp Asp Asn Gly Tyr Trp Trp Asp Met Leu Leu Val Thr Arg Phe Gly	
225 230 235 240	

acc ttc ctc aag aac aat tta ccg aca gcc atc tct gac tgg ttg tac	768
Thr Phe Leu Lys Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr	
245 250 255	
gtg aag cag atg aat gca aga ttc aag cat gaa aac tat ggc ttg atg	816
Val Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met	
260 265 270	
cct tta aat gga gtc ctg agg aaa gag cct gta ttt aac gat gag ctc	864
Pro Leu Asn Gly Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu	
275 280 285	
cca gca agc att ctg tgt ggc att gtg tcc gta aag cct aac gtg aag	912
Pro Ala Ser Ile Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys	
290 295 300	
gaa ttc aca gag acc tcg gcc att ttt gag gat ggg acc ata ttt gag	960
Glu Phe Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly Thr Ile Phe Glu	
305 310 315 320	
ggc att gac tgt gta atc ttt gca aca ggg tat agt ttt gcc tac ccc	1008
Gly Ile Asp Cys Val Ile Phe Ala Thr Gly Tyr Ser Phe Ala Tyr Pro	
325 330 335	
ttc ctt gat gag tct atc atc aaa agc aga aac aat gag atc att tta	1056
Phe Leu Asp Glu Ser Ile Ile Lys Ser Arg Asn Asn Glu Ile Ile Leu	
340 345 350	
ttt aaa gga gta ttt cct cct cta ctt gag aag tca acc ata gca gtg	1104
Phe Lys Gly Val Phe Pro Pro Leu Leu Glu Lys Ser Thr Ile Ala Val	
355 360 365	
att ggc ttt gtc cag tcc ctt ggg gct gcc att ccc aca gtt gac ctc	1152
Ile Gly Phe Val Gln Ser Leu Gly Ala Ala Ile Pro Thr Val Asp Leu	
370 375 380	
cag tcc cgc tgg gca gca caa gta ata aag gga act tgt act ttg cct	1200
Gln Ser Arg Trp Ala Ala Gln Val Ile Lys Gly Thr Cys Thr Leu Pro	
385 390 395 400	
tct atg gaa gac atg atg aat gat att aat gag aaa atg gag aaa aag	1248
Ser Met Glu Asp Met Met Asn Asp Ile Asn Glu Lys Met Glu Lys Lys	
405 410 415	
cgc aaa tgg ttt ggc aaa agc gag acc ata cag aca gat tac att gtt	1296
Arg Lys Trp Phe Gly Lys Ser Glu Thr Ile Gln Thr Asp Tyr Ile Val	
420 425 430	

tat atg gat gaa ctc tcc tcc ttc att ggg gca aag ccc aac atc cca	1344
Tyr Met Asp Glu Leu Ser Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro	
435 440 445	

tgg ctg ttt ctc aca gat ccc aaa ttg gcc atg gaa gtt tat ttt ggc	1392
Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Met Glu Val Tyr Phe Gly	
450 455 460	

cct tgt agt ccc tac cag ttt agg ctg gtg ggc cca ggg cag tgg cca	1440
Pro Cys Ser Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Gln Trp Pro	
465 470 475 480	

gga gcc aga aat gcc ata ctg acc cag tgg gac cgg tcg ttg aaa ccc	1488
Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro	
485 490 495	

atg cag aca cga gtg gtc ggg aga ctt cag aag cct tgc ttc ttt ttc	1536
Met Gln Thr Arg Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe	
500 505 510	

cat tgg ctg aag ctc ttt gca att cct att ctg tta atc gct gtt ttc	1584
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ctt gtg ttg acc taa	1599
Leu Val Leu Thr	
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<210> 6
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 <212> PRT
 <213> Homo sapiens

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20 25 30																	
Lys Ser Asn Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Ala Glu																	
35 40 45																	
Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys																	
50 55 60																	
Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn																	
65 70 75 80																	
Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys																	
85 90 95																	
Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser																	

				485					490					495			
Met	Gln	Thr	Arg	Val	Val	Gly	Arg	Leu	Gln	Lys	Pro	Cys	Phe	Phe	Phe		
			500					505					510				
His	Trp	Leu	Lys	Leu	Phe	Ala	Ile	Pro	Ile	Leu	Leu	Ile	Ala	Val	Phe		
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Leu	Val	Leu	Thr														
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 <213> Homo sapiens

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tcc	atc	agg	agc	tgt	ctg	gaa	gag	ggg	ctg	gag	ccc	acc	tgc	ttt	gag	96
Ser	Ile	Arg	Ser	Cys	Leu	Glu	Glu	Gly	Leu	Glu	Pro	Thr	Cys	Phe	Glu	
			20					25					30			
aag	agc	aat	gac	att	ggg	ggc	ctg	tgg	aaa	ttt	tca	gac	cat	gca	gag	144
Lys	Ser	Asn	Asp	Ile	Gly	Gly	Leu	Trp	Lys	Phe	Ser	Asp	His	Ala	Glu	
		35					40					45				
gag	ggc	agg	gct	agc	att	tac	aaa	tca	gtc	ttt	tcc	aac	tct	tcc	aaa	192
Glu	Gly	Arg	Ala	Ser	Ile	Tyr	Lys	Ser	Val	Phe	Ser	Asn	Ser	Ser	Lys	
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Phe	Met	His	Asn	Ser	Lys	Ile	Gln	Glu	Tyr	Ile	Ile	Ala	Phe	Ala	Lys	
				85				90						95		
gaa	aag	aac	ctc	ctg	aag	tac	ata	caa	ttt	aag	aca	ttt	gta	tcc	agt	336
Glu	Lys	Asn	Leu	Leu	Lys	Tyr	Ile	Gln	Phe	Lys	Thr	Phe	Val	Ser	Ser	
		100						105					110			

gta aat aaa cat cct gat ttt gca act act ggc cag tgg gat gtt acc	384
Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr	
115 120 125	
act gaa agg gat ggt aaa aaa gaa tcg gct gtc ttt gat gct gta atg	432
Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met	
130 135 140	
gtt tgt tcc gga cat cat gtg tat ccc aac cta cca aaa gag tcc ttt	480
Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Glu Ser Phe	
145 150 155 160	
cca gga cta aac cac ttt aaa ggc aaa tgc ttc cac agc agg gac tat	528
Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr	
165 170 175	
aaa gaa cca ggt gta ttc aat gga aag cgt gtc ctg gtg gtt ggc ctg	576
Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu	
180 185 190	
ggg aat tcg ggc tgt gat att gcc aca gaa ctc agc cgc aca gca gaa	624
Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu	
195 200 205	
cag gtc atg atc agt tcc aga agt ggc tcc tgg gtg atg agc cgg gtc	672
Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val	
210 215 220	
tgg gac aat ggt tat cct tgg gac atg ctg ctc gtc act cga ttt gga	720
Trp Asp Asn Gly Tyr Pro Trp Asp Met Leu Leu Val Thr Arg Phe Gly	
225 230 235 240	
acc ttc ctc aag aac aat tta ccg aca gcc atc tct gac tgg ttg tac	768
Thr Phe Leu Lys Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr	
245 250 255	
gtg aag cag atg aat gca aga ttc aag cat gaa aac tat ggc ttg atg	816
Val Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met	
260 265 270	
cct tta aat gga gtc ctg agg aaa gag cct gta ttt aac gat gag ctc	864
Pro Leu Asn Gly Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu	
275 280 285	
cca gca agc att ctg tgt ggc att gtg tcc gta aag cct aac gtg aag	912
Pro Ala Ser Ile Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys	
290 295 300	

gaa ttc aca gag acc tcg gcc att ttt gag gat ggg acc ata ttt gag	960
Glu Phe Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly Thr Ile Phe Glu	
305 310 315 320	
ggc att gac tgt gta atc ttt gca aca ggg tat agt ttt gcc tac ccc	1008
Gly Ile Asp Cys Val Ile Phe Ala Thr Gly Tyr Ser Phe Ala Tyr Pro	
325 330 335	
ttc ctt gat gag tct atc atc aaa agc aga aac aat gag atc att tta	1056
Phe Leu Asp Glu Ser Ile Ile Lys Ser Arg Asn Asn Glu Ile Ile Leu	
340 345 350	
ttt aaa gga gta ttt cct cct cta ctt gag aag tca acc ata gca gtg	1104
Phe Lys Gly Val Phe Pro Pro Leu Leu Glu Lys Ser Thr Ile Ala Val	
355 360 365	
att ggc ttt gtc cag tcc ctt ggg gct gcc att ccc aca gtt gac ctc	1152
Ile Gly Phe Val Gln Ser Leu Gly Ala Ala Ile Pro Thr Val Asp Leu	
370 375 380	
cag tcc cgc tgg gca gca caa gta ata aag gga act tgt act ttg cct	1200
Gln Ser Arg Trp Ala Ala Gln Val Ile Lys Gly Thr Cys Thr Leu Pro	
385 390 395 400	
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Ser Met Glu Asp Met Met Asn Asp Ile Asn Glu Lys Met Glu Lys Lys	
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Arg Lys Trp Phe Gly Lys Ser Glu Thr Ile Gln Thr Asp Tyr Ile Val	
420 425 430	
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Tyr Met Asp Glu Leu Ser Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro	
435 440 445	
tgg ctg ttt ctc aca gat ccc aaa ttg gcc atg gaa gtt tat ttt ggc	1392
Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Met Glu Val Tyr Phe Gly	
450 455 460	
cct tgt agt ccc tac cag ttt agg ctg gtg ggc cca ggg cag tgg cca	1440
Pro Cys Ser Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Gln Trp Pro	
465 470 475 480	
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Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro	
485 490 495	

atg cag aca cga gtg gtc ggg aga ctt cag aag cct tgc ttc ttt ttc 1536
 Met Gln Thr Arg Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe
 500 505 510

cat tgg ctg aag ctc ttt gca att cct att ctg tta atc gct gtt ttc 1584
 His Trp Leu Lys Leu Phe Ala Ile Pro Ile Leu Leu Ile Ala Val Phe
 515 520 525

ctt gtg ttg acc taa 1599
 Leu Val Leu Thr
 530

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 35 40 45
 Glu Gly Arg Ala Ser Ile Tyr Lys Ser Val Phe Ser Asn Ser Ser Lys
 50 55 60
 Glu Met Met Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn
 65 70 75 80
 Phe Met His Asn Ser Lys Ile Gln Glu Tyr Ile Ile Ala Phe Ala Lys
 85 90 95
 Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Phe Val Ser Ser
 100 105 110
 Val Asn Lys His Pro Asp Phe Ala Thr Thr Gly Gln Trp Asp Val Thr
 115 120 125
 Thr Glu Arg Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met
 130 135 140
 Val Cys Ser Gly His His Val Tyr Pro Asn Leu Pro Lys Glu Ser Phe
 145 150 155 160
 Pro Gly Leu Asn His Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr
 165 170 175
 Lys Glu Pro Gly Val Phe Asn Gly Lys Arg Val Leu Val Val Gly Leu
 180 185 190
 Gly Asn Ser Gly Cys Asp Ile Ala Thr Glu Leu Ser Arg Thr Ala Glu
 195 200 205
 Gln Val Met Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val
 210 215 220
 Trp Asp Asn Gly Tyr Pro Trp Asp Met Leu Leu Val Thr Arg Phe Gly

225		230		235		240
Thr Phe Leu Lys	Asn Asn Leu Pro Thr Ala Ile Ser Asp Trp Leu Tyr					
	245		250		255	
Val Lys Gln Met	Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met					
	260		265		270	
Pro Leu Asn Gly	Val Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu					
	275		280		285	
Pro Ala Ser Ile	Leu Cys Gly Ile Val Ser Val Lys Pro Asn Val Lys					
	290		295		300	
Glu Phe Thr Glu	Thr Ser Ala Ile Phe Glu Asp Gly Thr Ile Phe Glu					
305		310		315		320
Gly Ile Asp Cys	Val Ile Phe Ala Thr Gly Tyr Ser Phe Ala Tyr Pro					
	325		330		335	
Phe Leu Asp Glu	Ser Ile Ile Lys Ser Arg Asn Asn Glu Ile Ile Leu					
	340		345		350	
Phe Lys Gly Val	Phe Pro Pro Leu Leu Glu Lys Ser Thr Ile Ala Val					
	355		360		365	
Ile Gly Phe Val	Gln Ser Leu Gly Ala Ala Ile Pro Thr Val Asp Leu					
	370		375		380	
Gln Ser Arg Trp	Ala Ala Gln Val Ile Lys Gly Thr Cys Thr Leu Pro					
385		390		395		400
Ser Met Glu Asp	Met Met Asn Asp Ile Asn Glu Lys Met Glu Lys Lys					
	405		410		415	
Arg Lys Trp Phe	Gly Lys Ser Glu Thr Ile Gln Thr Asp Tyr Ile Val					
	420		425		430	
Tyr Met Asp Glu	Leu Ser Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro					
	435		440		445	
Trp Leu Phe Leu	Thr Asp Pro Lys Leu Ala Met Glu Val Tyr Phe Gly					
	450		455		460	
Pro Cys Ser Pro	Tyr Gln Phe Arg Leu Val Gly Pro Gly Gln Trp Pro					
	465		470		475	
Gly Ala Arg Asn	Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro					
	485		490		495	
Met Gln Thr Arg	Val Val Gly Arg Leu Gln Lys Pro Cys Phe Phe Phe					
	500		505		510	
His Trp Leu Lys	Leu Phe Ala Ile Pro Ile Leu Leu Ile Ala Val Phe					
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Leu Val Leu Thr						
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<212> DNA

<213> Homo sapiens

<400> 9

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7

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<212> DNA

<213> Homo sapiens

<400> 10

attaaa

6

<210> 11

<211> 6

<212> DNA

<213> Homo sapiens

<400> 11

aataaa

6

<210> 12

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HLFM03 -
Putative FAD binding domain.

<400> 12

Gly Ala Gly Val Ser Gly

1

5

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NADP+ binding
domain HLFM03

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1

5

<210> 14
 <211> 35
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: HFMO 3 cDNA
 primer

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 <210> 15
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HFM 3 cDNA
 primer

 <400> 15
 gggaagaaag tggccatc 18

 <210> 16
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HFMO 3
 oligonucleotide

 <400> 16
 ccggtcgacg gatccaagct taggtcaaca caagg 35

 <210> 17
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HFMO 3
 oligonucleotide

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cctggaaaagg actgttttgg taggttggg

29

<210> 18

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<212> DNA

<213> Artificial Sequence

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oligonucleotide

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29

219
cont